

Figure S2. Phylogenetic analysis of group B-type MAPKs from different species. The unrooted tree was constructed with a maximum likelihood method on the basis of the alignment of protein sequences and confirmation of the tree topology by bootstrap analysis (1000 replicates) were performed with MEGA software (default settings except the replicates of the bootstrap value). Species acronyms are included before the protein name: Ac, *Ananas comosus*; At, *Arabidopsis thaliana*; Bd, *Brachypodium distachyon*; Bn, *Brassica napus*; Cp, *Carica papaya*; Ga, *Gossypium arboreum*; Gm, *Glycine max*; Ha, *Helianthus annuus*; Na, *Nicotiana attenuata*; Nt, *Nicotiana tabacum*; Os, *Oryza sativa*; Pc, *Petroselinum crispum*; Pt, *Populus trichocarpa*; Sb, *Sorghum bicolor*; Si, *Setaria italica*; St, *Solanum tuberosum*; Zm, *Zea mays*. The scale bar represents 0.05 amino acid substitutions per site in the primary structure. Sequence data in the phylogenetic tree can be found in the GenBank/EMBL data libraries under accession numbers: AcMPK2 (XP_020080580.1); AtMPK4 (NP_192046.1); AtMPK5 (NP_567378.4); AtMPK11 (NP_001117210.1); BdMPK6 (XP_003574247.1); BnMPK4 (NP_001303223.1); CpMPK4 (XP_021887822.1); GaMPK4 (KHG15311.1); GmMPK4a (NP_001339892.1); GmMPK4b (NP_001242364.2); HaMPK4 (XP_021969289.1); NaMPK4 (ABO65100.1); NtMPK4 (NP_001312502.1); NtNRK1 (BAB32406.1); OsMPK4 (XP_015615011.1); PcMPK4 (AAN65180.1); PtMPK4 (XP_002302599.1); SbMPK6 (XP_002467591.1); SiMPK6 (XP_004983829.1); StMPK4 (BAB93529.1); ZmMPK1 (AIX47138.1); ZmMPK4 (BAA74733.1); ZmSIMK1 (NP_001105239.2). The diamond indicates the gene OsMPK4 that is characterized in this paper.

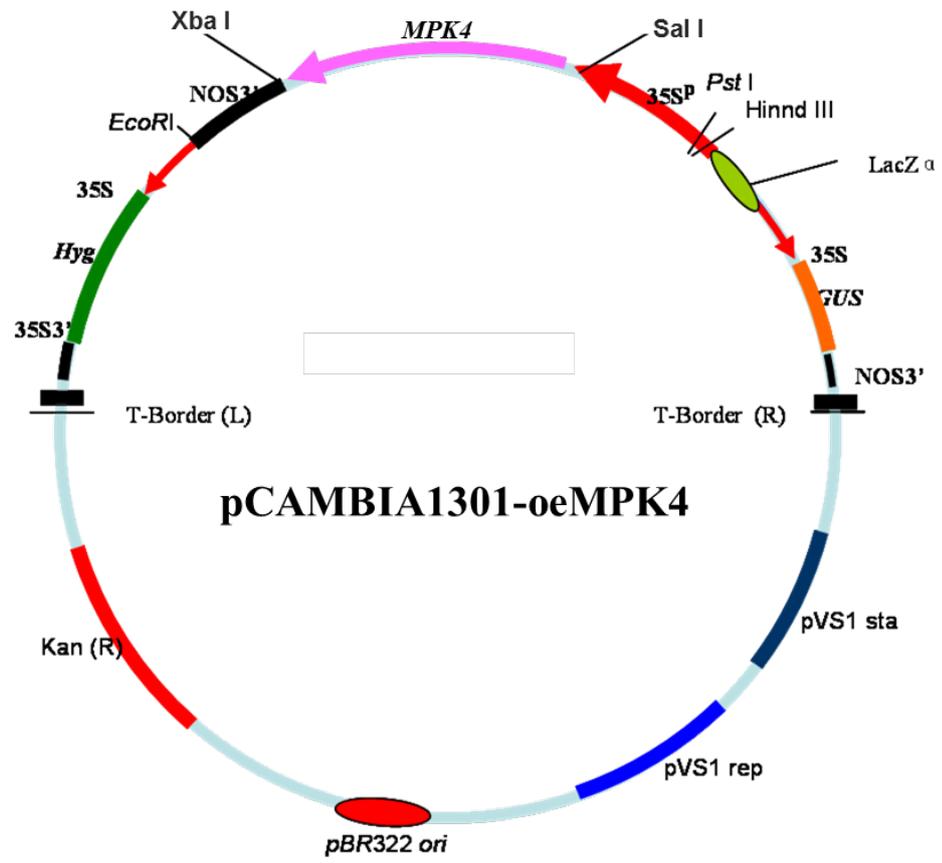


Figure S3. Transformation vector used in this study